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SEQUENCE LISTING

Millennium Pharmaceuticals, Inc.
Meyers, Rachel

<120> 27419, A NOVEL HUMAN ARGININE-N-METHYL
TRANSFERASE AND USES THEREOF

<130> 38155-20039.00

<140> US 09/970,638

<141> 2001-10-03

<150> US 60/237,717

<151> 2000-10-05

<160> 9

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 1201

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (34)...(1161)

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Met Ser Gln Pro Lys Lys Arg
1 5

aag ctt gag tcg ggg ggc ggc ggc gaa gga ggg gag gga act gaa gag 102
Lys Leu Glu Ser Gly Gly Gly Glu Gly Gly Glu Gly Thr Glu Glu
10 15 20

gaa gat ggc gcg gag cgg gag gcg gcc ctg gag cga ccc cgg agg act 150
Glu Asp Gly Ala Glu Arg Glu Ala Ala Leu Glu Arg Pro Arg Arg Thr
25 30 35

aag cgg gaa cgg gac cag ctg tac tac gag tgc tac tcg gac gtt tcg 198
Lys Arg Glu Arg Asp Gln Leu Tyr Tyr Glu Cys Tyr Ser Asp Val Ser
40 45 50 55

gtc cac gag gag atg atc gcg gac cgc gtc cgc acc gat gcc tac cgc 246
Val His Glu Glu Met Ile Ala Asp Arg Val Arg Thr Asp Ala Tyr Arg
60 65 70

ctg ggt atc ctt cgg aac tgg gca gca ctg cga ggc aag acg gta ctg 294
Leu Gly Ile Leu Arg Asn Trp Ala Ala Leu Arg Gly Lys Thr Val Leu
75 80 85

gac gtg ggc gcg ggc acc ggc att ctg agc atc ttc tgt gcc cag gcc 342
Asp Val Gly Ala Gly Thr Gly Ile Leu Ser Ile Phe Cys Ala Gln Ala

| 90 | 95 | 100 | |
|---|-----|-----|------|
| ggg gcc cgg cgc gtg tac gcg gta gag gcc agc gcc atc tgg caa cag | | | 390 |
| Gly Ala Arg Arg Val Tyr Ala Val Glu Ala Ser Ala Ile Trp Gln Gln | | | |
| 105 | 110 | 115 | |
| gcc cgg gag gtg gtg cgg ttc aac ggg ctg gag gac cgg gtg cac gtc | | | 438 |
| Ala Arg Glu Val Val Arg Phe Asn Gly Leu Glu Asp Arg Val His Val | | | |
| 120 | 125 | 130 | 135 |
| ctg ccg gga cca gtg gag act gta gag ttg ccg gaa cag gtg gat gcc | | | 486 |
| Leu Pro Gly Pro Val Glu Thr Val Glu Leu Pro Glu Gln Val Asp Ala | | | |
| 140 | 145 | 150 | |
| atc gtg agc gag tgg atg ggc tac gga ctc ctg cac gag tcc atg ctg | | | 534 |
| Ile Val Ser Glu Trp Met Gly Tyr Gly Leu Leu His Glu Ser Met Leu | | | |
| 155 | 160 | 165 | |
| agc tcc gtc ctc cac gcg cga acc aag tgg ctg aag gag ggc ggt ctt | | | 582 |
| Ser Ser Val Leu His Ala Arg Thr Lys Trp Leu Lys Glu Gly Gly Leu | | | |
| 170 | 175 | 180 | |
| ctc ctg ccg gcc tcc gcc gag ctc ttc ata gcc ccc atc agc gac cag | | | 630 |
| Leu Leu Pro Ala Ser Ala Glu Leu Phe Ile Ala Pro Ile Ser Asp Gln | | | |
| 185 | 190 | 195 | |
| atg ctg gaa tgg cgc ctg ggc ttc tgg agc cag gtg aag cag cac tat | | | 678 |
| Met Leu Glu Trp Arg Leu Gly Phe Trp Ser Gln Val Lys Gln His Tyr | | | |
| 200 | 205 | 210 | 215 |
| ggg gtg gac atg agc tgc ctg gag ggc ttc gcc acg cgc tgt ctc atg | | | 726 |
| Gly Val Asp Met Ser Cys Leu Glu Gly Phe Ala Thr Arg Cys Leu Met | | | |
| 220 | 225 | 230 | |
| ggc cac tcg gag atc gtt gtg cag gga ttg tcc ggc gag gac gtg ctg | | | 774 |
| Gly His Ser Glu Ile Val Val Gln Gly Leu Ser Gly Glu Asp Val Leu | | | |
| 235 | 240 | 245 | |
| gcc cgg ccg cag cgc ttt gct cag cta gag ctc tcc cgc gcc ggc ttg | | | 822 |
| Ala Arg Pro Gln Arg Phe Ala Gln Leu Glu Leu Ser Arg Ala Gly Leu | | | |
| 250 | 255 | 260 | |
| gag cag gag ctg gag gcc gga gtg ggc ggg cgc ttc cgc tgc agc tgc | | | 870 |
| Glu Gln Glu Leu Glu Ala Gly Val Gly Gly Arg Phe Arg Cys Ser Cys | | | |
| 265 | 270 | 275 | |
| tat ggc tcg gcg ccc atg cat ggc ttt gcc atc tgg ttc cag gtg acc | | | 918 |
| Tyr Gly Ser Ala Pro Met His Gly Phe Ala Ile Trp Phe Gln Val Thr | | | |
| 280 | 285 | 290 | 295 |
| ttc cct gga ggg gag tcg gag aaa ccc ctg gtg ctg tcc acc tcg cct | | | 966 |
| Phe Pro Gly Gly Glu Ser Glu Lys Pro Leu Val Leu Ser Thr Ser Pro | | | |
| 300 | 305 | 310 | |
| ttt cac ccg gcc act cac tgg aaa cag gcg ctc ctc tac ctg aac gag | | | 1014 |
| Phe His Pro Ala Thr His Trp Lys Gln Ala Leu Leu Tyr Leu Asn Glu | | | |
| 315 | 320 | 325 | |

ccg gtg caa gtg gag caa gac acg gac gtt tca gga gag atc acg ctg 1062
 Pro Val Gln Val Glu Gln Asp Thr Asp Val Ser Gly Glu Ile Thr Leu
 330 335 340

ctg ccc tcc cgg cac aac ccc cgt cgc ctg cgc gtg ctg ctg cgc tac 1110
 Leu Pro Ser Arg His Asn Pro Arg Arg Leu Arg Val Leu Leu Arg Tyr
 345 350 355

aaa gtg gga gac cag gag gag aag acc aaa gac ttt gcc atg gag gac 1158
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 360 365 370 375

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 <212> PRT
 <213> Homo sapiens

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 Leu Glu Arg Pro Arg Arg Thr Lys Arg Glu Arg Asp Gln Leu Tyr Tyr
 35 40 45
 Glu Cys Tyr Ser Asp Val Ser Val His Glu Glu Met Ile Ala Asp Arg
 50 55 60
 Val Arg Thr Asp Ala Tyr Arg Leu Gly Ile Leu Arg Asn Trp Ala Ala
 65 70 75 80
 Leu Arg Gly Lys Thr Val Leu Asp Val Gly Ala Gly Thr Gly Ile Leu
 85 90 95
 Ser Ile Phe Cys Ala Gln Ala Gly Ala Arg Arg Val Tyr Ala Val Glu
 100 105 110
 Ala Ser Ala Ile Trp Gln Gln Ala Arg Glu Val Val Arg Phe Asn Gly
 115 120 125
 Leu Glu Asp Arg Val His Val Leu Pro Gly Pro Val Glu Thr Val Glu
 130 135 140
 Leu Pro Glu Gln Val Asp Ala Ile Val Ser Glu Trp Met Gly Tyr Gly
 145 150 155 160
 Leu Leu His Glu Ser Met Leu Ser Ser Val Leu His Ala Arg Thr Lys
 165 170 175
 Trp Leu Lys Glu Gly Gly Leu Leu Leu Pro Ala Ser Ala Glu Leu Phe
 180 185 190
 Ile Ala Pro Ile Ser Asp Gln Met Leu Glu Trp Arg Leu Gly Phe Trp
 195 200 205
 Ser Gln Val Lys Gln His Tyr Gly Val Asp Met Ser Cys Leu Glu Gly
 210 215 220
 Phe Ala Thr Arg Cys Leu Met Gly His Ser Glu Ile Val Val Gln Gly
 225 230 235 240
 Leu Ser Gly Glu Asp Val Leu Ala Arg Pro Gln Arg Phe Ala Gln Leu
 245 250 255
 Glu Leu Ser Arg Ala Gly Leu Glu Gln Glu Leu Glu Ala Gly Val Gly

Lys Gly Gly Glu Glu Asp Phe Glu Gly Leu Leu Gly Glu Gly Tyr Gly
 50 55 60
 Ile Thr Gly Glu Tyr Arg Thr Arg Arg Glu Leu Leu Ala Gly Glu Lys
 65 70 75 80
 Asp Ser Gly Glu Thr Val Thr Ile His Lys Glu Asn Gly Cys Arg Phe
 85 90 95
 Lys Leu Asp Val Ser Lys Val Tyr Phe Ser Pro Arg Leu Glu Gly Glu
 100 105 110
 Arg Glu Arg Leu Ala Lys Leu Val Lys Glu Gly Glu Val Val Val Asp
 115 120 125
 Met Phe Ala Gly Ile Gly Pro Phe Ser Ile Pro Ile Ala Lys His Ser
 130 135 140
 Lys Ala Lys Arg Val Tyr Ala Val Asp Leu Asn Pro Glu Ala Val Lys
 145 150 155 160
 Tyr Leu Lys Glu Asn Ile Lys Leu Asn Lys Val Glu Asp Gln Pro Lys
 165 170 175
 Ile Gln Thr Val Val Asn Lys Ile Ile Pro Ile Leu Gly Asp Val Arg
 180 185 190
 Glu Val Ile Pro Glu Lys Glu Ala Gly Val His Ser Leu Val Lys Leu
 195 200 205
 Val Val Ala Asp Arg Val Ile Met Pro Leu Pro Leu Ala Arg Val Gly
 210 215 220
 Gln Ile Ser Ala His Glu Phe Leu Asp Lys Ala Leu Arg Lys Val Lys
 225 230 235 240
 Asp Gly Gly Ile Leu Val Ser Val Ile His Tyr Tyr Glu Phe Leu Pro
 245 250 255
 Glu Lys Ala Ile Pro Phe Leu Pro Val Glu Arg Ile Lys Arg Ala Ala
 260 265 270
 Glu Lys Glu Gly Val Lys Val Glu Ile Leu Lys Lys Arg Lys Val Lys
 275 280 285
 Asn Tyr Ala Pro Gly Val Tyr His Val Val Leu Asp Ala Arg Val Asn
 290 295 300

<210> 5

<211> 185

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 5

Pro Asp Lys Cys Thr Leu His Leu Thr Ala Ile Glu Asp Thr Gln Tyr
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 Lys Asp Glu Lys Ile Asn Phe Trp Asp Asp Val Tyr Gly Phe Asx Met
 20 25 30
 Ser Cys Met Lys Asp Ala Ala Ile Lys Glu Pro Ile Val Asp Pro Lys
 35 40 45
 Tyr Asn His Val Val Asp Pro Asn Gln Ile Ile Thr Asp Pro Cys Thr
 50 55 60
 Ile Lys Glu Phe Asp Met His Thr Val Lys Ile Ser Asp Leu Glu Thr
 65 70 75 80
 Phe Thr Ser Pro Phe Lys Leu Thr Val Lys Arg Asn Gly Met Leu His
 85 90 95
 Ala Phe Thr Ala Trp Phe Asp Val Tyr Phe Thr Ser Lys Arg Cys His
 100 105 110
 Pro Ile Pro Glu Ala Ile Asp Lys Pro Val Gly Phe Ser Thr Gly Pro

115 120 125
 Gln Ser Pro Tyr Thr His Trp Lys Gln Thr Ile Phe Tyr Met Glu Asp
 130 135 140
 Pro Leu Pro Val Lys Thr Gly Asp Thr Ile Glu Gly Ser Ile Thr Ile
 145 150 155 160
 Ser Lys Asn Lys Lys Asn Asn Arg Asp Leu Asp Ile Thr Leu Ser Trp
 165 170 175
 Asn Val Asn Gly Arg Gln Asp Pro Thr
 180 185

<210> 6
 <211> 129
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 6
 His Ile Arg Met Ile Asn Asp Val Lys Arg Asn Glu Ala Phe Ala Lys
 1 5 10 15
 Ala Leu Asn Asp Thr Ile Lys Ser Arg Ile Thr Val Val Phe Asp Ile
 20 25 30
 Gly Ser Gly Thr Gly Ile Leu Ser Ala Ile Ala Ala Arg Lys Thr Asn
 35 40 45
 Leu Val Thr Ala Leu Glu Glu Asn Met Cys Leu Thr Met Ile Ser Lys
 50 55 60
 Glu Val Leu Lys Arg Asn Gly Val Glu Ser Arg Val Asn Val His Ala
 65 70 75 80
 Lys Asn Ser Thr Tyr Phe Glu Thr Cys Glu Lys Ala Asp Ile Val Val
 85 90 95
 Ser Glu Thr Leu Asp Cys Cys Val Phe Gly Glu Lys Ile Val Glu Thr
 100 105 110
 Phe Leu Asp Ala His Val Arg Phe Ser His Asp Arg Thr Ile Phe Ile
 115 120 125
 Pro

<210> 7
 <211> 38
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Consensus amino acid sequence

<400> 7
 Lys Thr Asp Glu Asp Tyr Tyr Tyr Phe Asp Ser Tyr Ala His Tyr Gly
 1 5 10 15
 Ile His Glu Glu Met Leu Lys Asp Ser Val Arg Thr Glu Ser Tyr Arg
 20 25 30
 Asp Phe Ile Tyr His Asn
 35

<210> 8
 <211> 39
 <212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 8

Gln Asp Glu Glu Tyr Phe Gly Ser Tyr Gly Thr Leu Lys Leu His Leu
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Glu Met Leu Ala Asp Gln Pro Arg Thr Thr Lys Tyr His Ser Val Ile
20 25 30
Leu Gln Asn Lys Glu Ser Leu
35

<210> 9

<211> 196

<212> PRT

<213> Artificial Sequence

<220>

<223> Consensus amino acid sequence

<400> 9

Leu Arg Arg Gln Ala Ala Ile Arg Thr Asp Ser Leu Asp Val Gln Gly
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Leu Gly Ser Arg Glu Asp Leu Leu Ser Glu Val Ser Gly Pro Ser Cys
20 25 30
Pro Leu Thr Arg Ser Ser Ser Phe Trp Gly Gly Ser Ser Ile Gln Val
35 40 45
Gln Gln Arg Ser Gly Ile Gln Ser Lys Val Ser Lys His Ile Arg Leu
50 55 60
Pro Ala Pro Cys Pro Gly Leu Glu Pro Ser Trp Ala Lys Asp Pro Pro
65 70 75 80
Glu Thr Arg Ser Ser Leu Glu Leu Asp Thr Glu Leu Ser Trp Ile Ser
85 90 95
Gly Asp Leu Leu Pro Ser Ser Gln Glu Glu Pro Leu Phe Pro Arg Asp
100 105 110
Leu Lys Lys Cys Tyr Ser Val Glu Thr Gln Ser Cys Arg Arg Pro
115 120 125
Gly Phe Trp Leu Asp Glu Gln Arg Arg His Ser Ile Ala Val Ser Cys
130 135 140
Leu Asp Ser Gly Ser Gln Pro Arg Leu Cys Pro Ser Pro Ser Ser Leu
145 150 155 160
Gly Gly Gln Pro Leu Gly Gly Pro Gly Ser Arg Pro Lys Lys Lys Leu
165 170 175
Ser Pro Pro Ser Ile Ser Ile Asp Pro Pro Glu Ser Gln Gly Ser Arg
180 185 190
Pro Pro Cys Ser
195